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cons.aa	G G	G V	A K	E
hTGFBR-II	LDTLVGKGRFAEVYKAKLQNTSEQFETVAVKIFPYDHYASWKRKDIFPSDINLGHENILOF			
mActR-IIIB	LLEIKARGRGCCVWKAQLMN-----DFVAVKIKPLQDKQSWSEREIFSTPGMCHENILQF			
mActR-II	LLEVKGARGRGCCVWKAQLMN-----EVAVKIFPIQDKQSWSONEYEVSI PGCHENILQF			
daf-1	LTVRVGSGRFGNVSRGDYRG-----EAVAVKVFNAADEPAFHKEIEIFETRMLRHNPVLRY			
subdomains	I		II	III
				IV

hTGFBR-II	LTAEEERKTELCKQYWLITAFHAKGNLQEYLTRHVI SWEDLRNVGSSLARGLSHLHSDHTP-C					
mActR-IIIB	IAAEKRGSNLEVELWLITAFHDKGSLIDYLKGNI ITWNELCHVAETMSRCISYLMEDVPWCR					
mActR-II	ICAEKRGTSVDVDLWLITAFHEKGSLSDFLKANVSWNELCHIAETMARGCLAYLHEDIPGLK					
daf-1	IGSDRVDTGFVTELWLVIEYHPSGSILHDFFLLENTVNIEYYNLMRSTASGLAFLHNQIGGSK					
subdomains	V					VI-A

cons.aa	DLK N	DFG		
hTGFBR-II	-GRPKMPIVHRDLKSSNLVKNDLTCCLCDFGLSLRL---GPYSSVDDLANSQVGTARYMAP			
mActR-IIIB	GEHKPKSIAHRDFKSKNVLLKSDLTAVLADFGLAVERF---EPGKPPGD--THGQVGTRRYMAP			
mActR-II	-DGHKPAAISHRDIKSKNVLNNLTACIADFGLALKF---EAGKSAGD--THGQVGTRRYMAP			
daf-1	-ESNKPAMAHRIKSTQNTMYKNDLTCAIIDLGLSLSKPEDAASDIAN--ENYKCGTVRYLAP			
subdomains	VI-B	VII	VIII	

Fig. 1

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a.a C C E G N M C
5' GCGGATCCTGGTGTGAAGGNAATATGTG 3' Fig. 2A
BAMHI C C G C

a.a V A V K I F
5' GCGGATCCGTCGCAGTCAAAATT 3' Fig. 2B
BamHI G C G G C
T T T A

a.a R D I K S K N
5' GCGGATCCGCCATATTAAAAGCAA 3' Fig. 2C
BAMHI A C C GTCT
G A

a.a E P A M Y
5' CGGAATTCTGGTGCCATATA Fig. 2D
EcoRI G G G
A A

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M C G A A K L A F A V F I S C S S C A I L C R A C C R - 11
M T A P M A A L A L L M C S [REDACTED] C R C E A C C R - 110
M C A C L L R G L W P L H I V L W T R I A S T I P H E [REDACTED] C A V T E R - 11
M E A A A A Q K S V N N O M I V T O N N C A V T E R - 11
M E A A A A Q K S V N N O M I V T O N N C A V T E R - 1 / A L K - S
M T L G S P R K C U [REDACTED] L M L L H A L V A L K - 1
M Y D C V M I L P Y [REDACTED] I M I A L P S P A L K - 2
M S M L H G T G M K S O S O Q K K S E A L K - 3
M T L L R S S C K L H V G T K K E A L K - 4
M T Q L Y I Y I R L L G A Y L F I I S R V Q C Q H L D S M [REDACTED] F P L V Y L L A L K - 5

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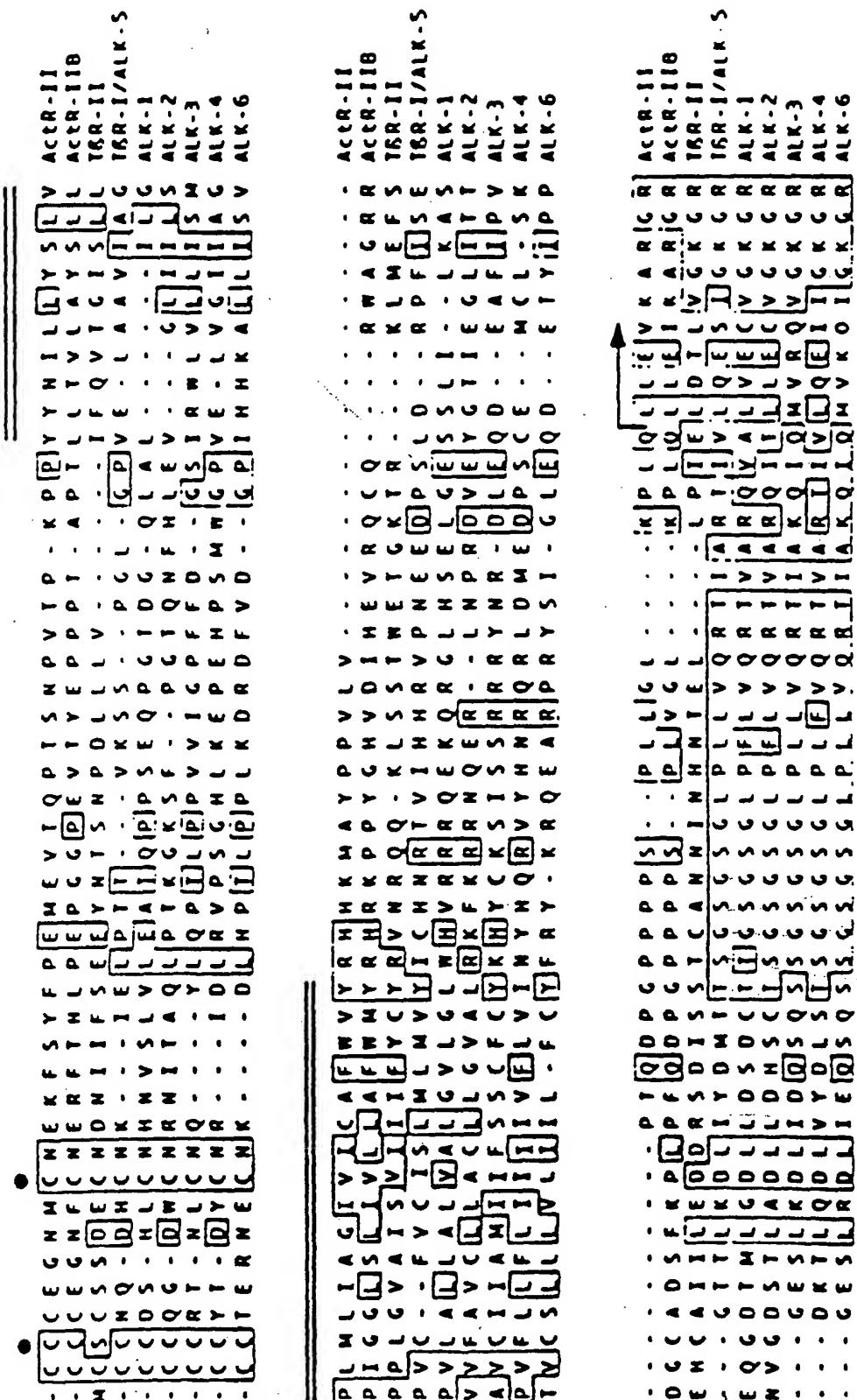


Fig. 3 contd.

Fig. 3 contd.

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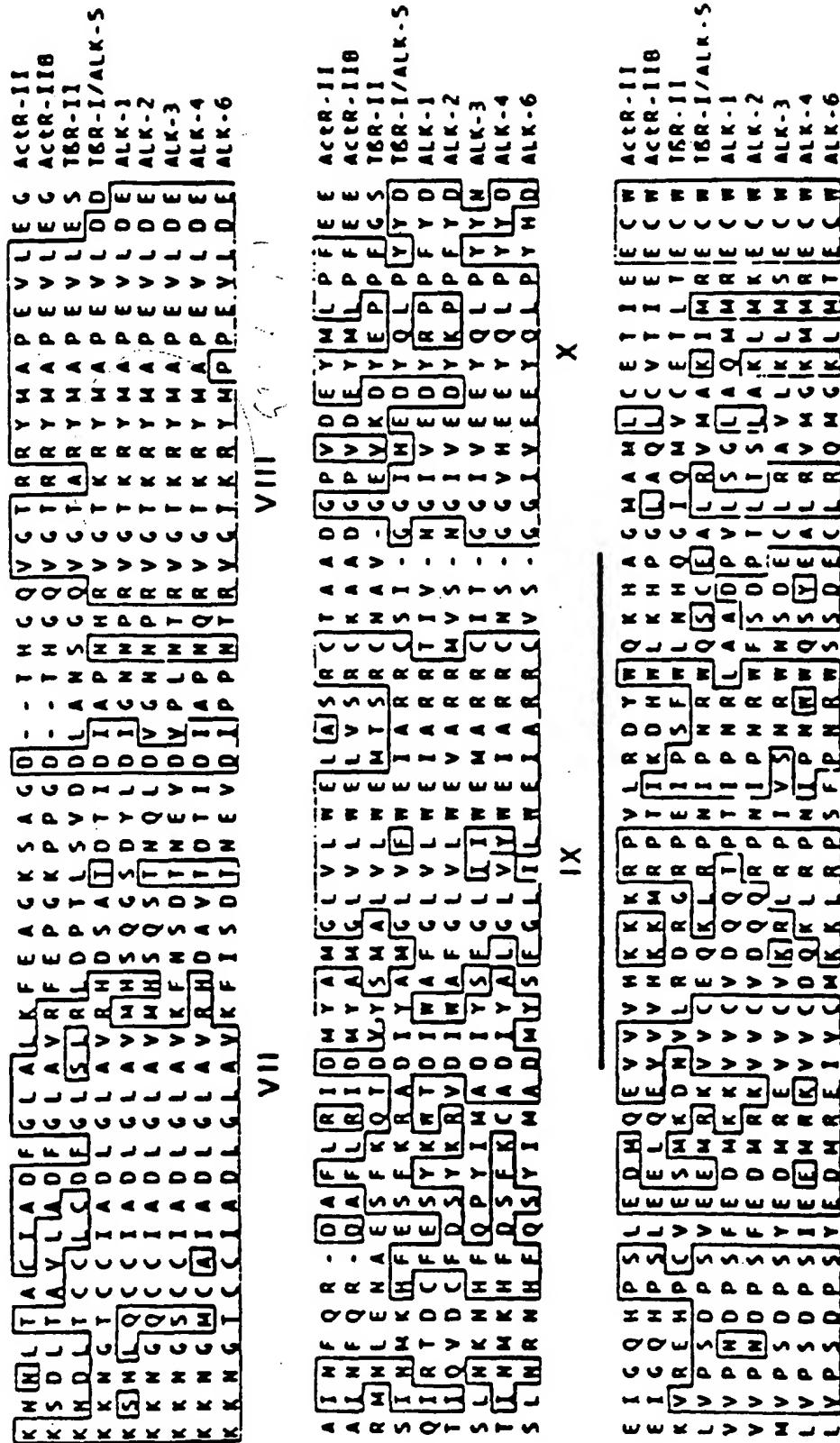


Fig. 3 contd.

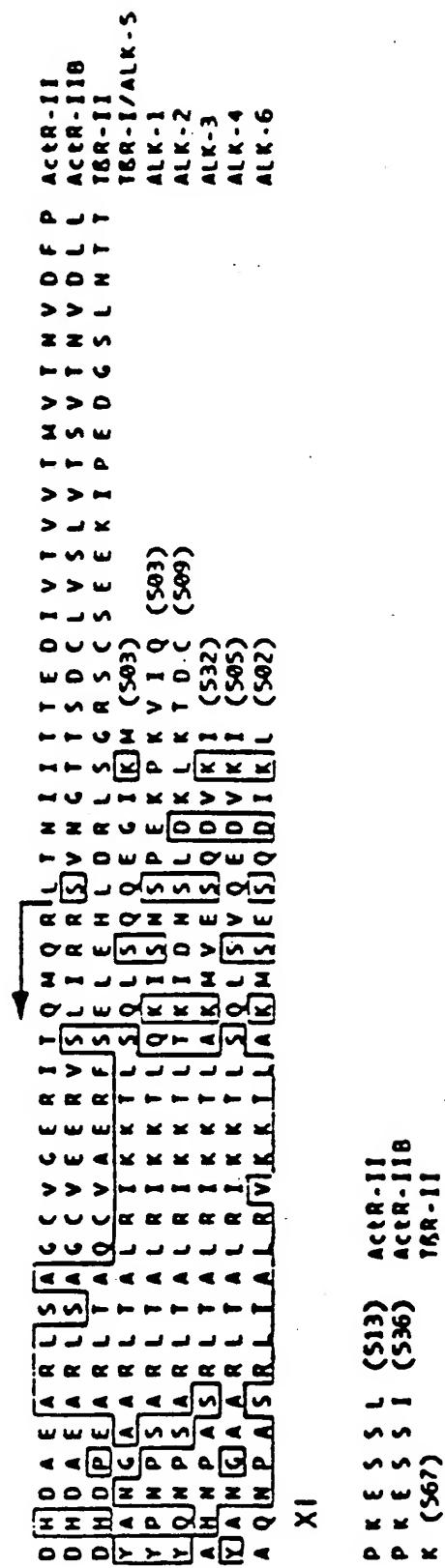
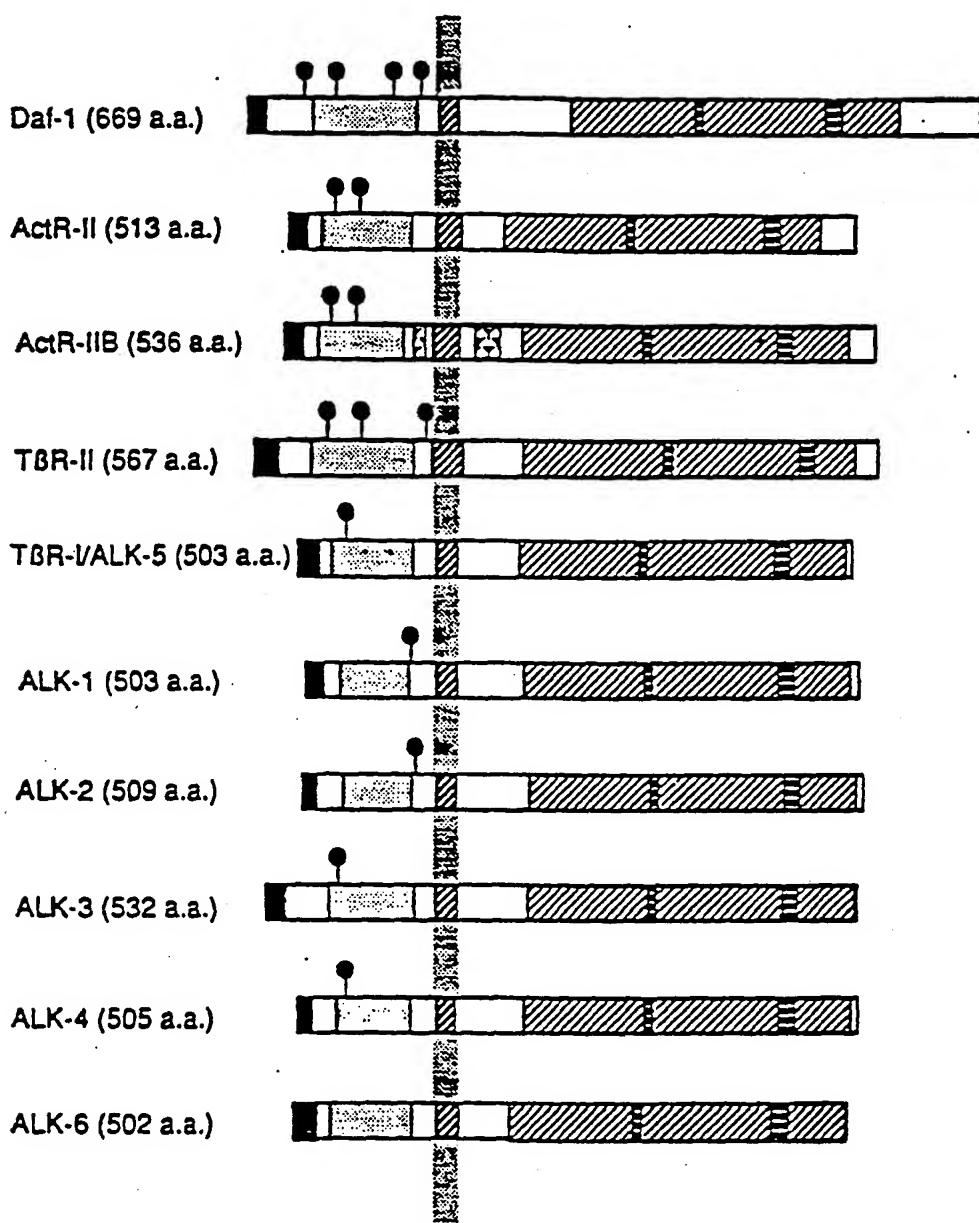


Fig. 3 contd.



- | | | | |
|--|--------------------------------|--|--------------------------------|
| | signal sequence | | insert in the kinase domain |
| | cysteine-rich region | | potential N-glycosylation site |
| | transmembrane domain | | alternatively spliced region |
| | serine/threonine kinase domain | | |

Fig. 4

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C - F - - C - - C X G D - D I - - T C E T - - G - C F V S L - - S D G Majority

C - T - - C E S P - - V - - C E G L - - S C G P - - H C K G P - - S C C G N E D H C E G O O - - T C R - - G A W C T Y V E R E E G ALK-1/CR
 C - Y - - C S G - - U C T S - - C H L - - C L E F N - - A N M E K D R T N O S G L E R T N O S G L E R C E G E O D K R R H C F A T - - N K N I - - S G S ACTR-II/CR
 C - A - - C L I Y X N - - C D V R F S T - - C D V R F S T G W V P G I E F L N E T D R S F Y E N T - - C Y T D - G S C Y Q S A - - R P S D A F - 1 / C R

Majority

ALK-1/CR
 ALK-2/CR
 ALK-3/CR
 ALK-4/CR
 ALK-5/CR
 ACTR-II/CR
 ACTR-III/CR
 TBR-II/CR
 DAF-1/CR

R H P Q E H R G - - C G N L H - - C R G R P T E - - F V N H Y C - - C D S H L C
 F H V Y Q K G Q - - E Q G K M T C - - K T P P P S P Q O A D - - C O G D W C
 G E T T L A S G - - F O V X - - G S D F Q C K D S S E D - - K O L R R T I E C - - C R T N Y C
 M E H H V A R T C - - G N K Y E - - I P K Y E L U P A G K P F Y C A P S S K T G S V R T H C - - C Y T D Y C
 K V I T H N S N C - - I A E I D I L I P R D R P F V C U E K K D S P E - - V Y F C C C E G N M C
 I E J V K Q G C W L D D F N C Y D R O E - - C V A T E E N P Q - - Y Y F C C C E G N F C
 J E L L Y K K G C W L D D F N C Y D R O E - - D A A S P K C I M K E K K K P Q G E T F F M C C S S D E C
 N I T L E T Y C H D P K L P Y H D F I L E D A A S P K C I M K E K K K P Q G E T F F M C C S S D E C
 P E I S H F G C - - H D E K S V T D E T T E F H D T R A K V C T N N T K D P H A T Y W I C C D K G N F C

Fig. 5

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ALK-2	ALK-3	ALK-4	ALK-5	ActR-II	ActR-IIB	TBR-II	daf-1
79	60	61	63	40	40	37	39
	63	64	65	41	39	37	39
		63	65	41	38	37	39
			90	41	40	39	42
				42	40	41	43
					78	48	35
						47	32
							34

ALK-1
ALK-2
ALK-3
ALK-4
ALK-5
ActR-II
ActR-IIB
TBR-II

Fig. 6

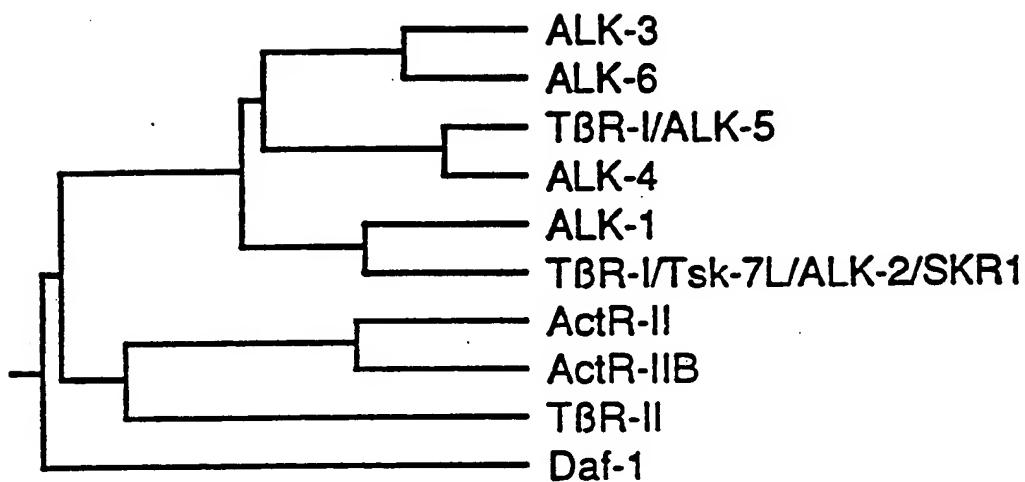


Fig. 7